Journal of MOLECULAR BIOLOGY

EDITOR-IN-CHIEF
J. C. KENDREW

ASSISTANT EDITOR
S. BRENNER

EDITORIAL BOARD
C. R. Cantor
P. Chambon
W. W. Franke
M. Gellert
G. A. Gilbert
M. Gottesman
I. Herskowitz
R. Huber
H. E. Huxley
A. Klug
V. Luzzati
J. H. Miller
M. F. Moody
K. Simons

VOLUME 174

25 March to 25 April 1984

ACADEMIC PRESS
London New York San Francisco

Copyright © 1984, by Academic Press Inc. (London) Ltd.

ALL RIGHTS RESERVED

No part of this volume may be reproduced in any form, by photostat, microfilm, or any other means, without written permission from the publishers.

Printed in Great Britain

CONTENTS OF VOLUME 174

Number 1, 25 March 1984

Blumenthal, T., Squire, M., Kirtland, S., Cane, J., Donegan, M., Spieth, J. and Sharrock, W., Cloning of a Yolk Protein Gene Family from *Caenorhabditis elegans* 1

Tahara, T., Kuroiwa, A., Obinata, M. and Natori, S., Multi-gene Structure of the Storage Protein Genes of *Sarcophaga peregrina* . . 19

Krolewski, J. J. and Rush, M. G., Some Extrachromosomal Circular DNAs Containing the *Alu* Family of Dispersed Repetitive Sequences May be Reverse Transcripts 31

Krolewski, J. J., Schindler, C. W. and Rush, M. G., Structure of Extrachromosomal Circular DNAs Containing Both the *Alu* Family of Dispersed Repetitive Sequences and Other Regions of Chromosomal DNA 41

Bullock, P., Forrester, W. and Botchan, M., DNA Sequence Studies of Simian Virus 40 Chromosomal Excision and Integration in Rat Cells . 55

Appendix: 82

Cabrera, C. V., Lee, J. J., Ellison, J. W., Britten, R. J. and Davidson, E. H., Regulation of Cytoplasmic mRNA Prevalence in Sea Urchin Embryos. Rates of Appearance and Turnover for Specific Sequences . 85

Inouye, S., Identification of a Development-specific Promoter of *Myxococcus xanthus* 113

Pruitt, S. C. and Reeder, R. H., Effect of Topological Constraint on Transcription of Ribosomal DNA in *Xenopus* Oocytes. Comparison of Plasmid and Endogenous Genes 121

Miroczka, D. H., Cassidy, B., Busch, H. and Rothblum, L. I., Characterization of Rat Ribosomal DNA. The Highly Repetitive Sequences that Flank the Ribosomal RNA Transcription Unit are Homologous and Contain RNA Polymerase III Transcription Initiation Sites 141

Flore, G. M., Gronenborn, A. M. and McLaughlin, L. W., Structure of the Ribotrinucleoside Diphosphate Codon UpUpC Bound to $tRNA^{Phe}$ from Yeast. A Time-dependent Transferred Nuclear Overhauser Enhancement Study 163

Lesk, A. M. and Chothia, C., Mechanisms of Domain Closure in Proteins . 175

Taylor, K., Dux, L. and Martonosi, A., Structure of the Vanadate-induced Crystals of Sarcoplasmic Reticulum Ca^{2+}-ATPase 193

Wiegand, G., Remington, S., Deisenhofer, J. and Huber, R., Crystal Structure Analysis and Molecular Model of a Complex of Citrate Synthase with Oxaloacetate and *S*-Acetonyl-coenzyme A 205

Letters to the Editor

Shindo, H., Fujiwara, T., Akutsu, H., Matsumoto, U. and Shimidzu, M., Multiple Conformations Coexist and Interchange in Natural *B* DNA Fibers. 221

Stewart, M., Crystalline Sheets of Tropomyosin 231

Poulsen, F. R. and Lowy, J., Application of Potential Energy Calculations to the Determination of Muscle Structure from X-ray Data with Special Reference to the Configuration of Myosin Heads 239

Errata 249

Number 2, 5 April 1984

Biel, S. W., Adelt, G. and Berg, D. E., Transcriptional Control of IS*1* Transposition in *Escherichia coli* 251

Ramakrishnan, V., Capel, M., Kjeldgaard, M., Engelman, D. M. and Moore, P. B., Positions of Proteins S14, S18 and S20 in the 30 S Ribosomal Subunit of *Escherichia coli* 265

Setyono, B. and Pederson, T., Ribonucleoprotein Organization of Eukaryotic RNA. XXX. Evidence that U1 Small Nuclear RNA is a Ribonucleoprotein when Base-paired with Pre-messenger RNA *in Vivo* 285

Gebhardt, A., Bosch, J. V., Ziemiecki, A. and Friis, R. R., Rous Sarcoma Virus p19 and gp35 can be Chemically Crosslinked to High Molecular Weight Complexes. An Insight into Virus Assembly 297

Wejman, J. C., Hovsepian, D., Wall, J. S., Hainfeld, J. F. and Greer, J., Structure of Haptoglobin and the Haptoglobin–Hemoglobin Complex by Electron Microscopy 319

Wejman, J. C., Hovsepian, D., Wall, J. S., Hainfeld, J. F. and Greer, J., Structure and Assembly of Haptoglobin Polymers by Electron Microscopy 343

Müller, M. F., Ris, H. and Ferry, J. D., Electron Microscopy of Fine Fibrin Clots and Fine and Coarse Fibrin Films. Observations of Fibers in Cross-section and in Deformed States 369

Sędzik, J., Blaurock, A. E. and Höchli, M., Lipid/Myelin Basic Protein Multilayers. A Model for the Cytoplasmic Space in Central Nervous System Myelin 385

LETTER TO THE EDITOR

STATES, D. J., DOBSON, C. M., KARPLUS, M. and CREIGHTON, T. E., A New Two-disulphide Intermediate in the Refolding of Reduced Bovine Pancreatic Trypsin Inhibitor 411

NUMBER 3, 15 APRIL 1984

SHARROCK, W. J., Cleavage of Two Yolk Proteins from a Precursor in *Caenorhabditis elegans* 419

KOCHAN, J., CARRASCOSA, J. L. and MURIALDO, H., Bacteriophage Lambda Preconnectors. Purification and Structure 433

MAKOWSKI, L., CASPAR, D. L. D., PHILLIPS, W. C. and GOODENOUGH, D. A., Gap Junction Structures. V. Structural Chemistry Inferred from X-ray Diffraction Measurements on Sucrose Accessibility and Trypsin Susceptibility 449

RICE, D. W., SCHULZ, G. E. and GUEST, J. R., Structural Relationship between Glutathione Reductase and Lipoamide Dehydrogenase . . 483

KIRSCH, J. F., EICHELE, G., FORD, G. C., VINCENT, M. G., JANSONIUS, J. N., GEHRING, H. and CHRISTEN, P., Mechanism of Action of Aspartate Aminotransferase Proposed on the Basis of its Spatial Structure . . 497

ROGERS, N. K. and STERNBERG, M. J. E., Electrostatic Interactions in Globular Proteins. Different Dielectric Models Applied to the Packing of α-Helices 527

Appendix: 540

LAURENT, M. and KELLERSHOHN, N., Apparent Co-operativity for Highly Concentrated Michaelian and Allosteric Enzymes 543

Appendix: 553

LETTER TO THE EDITOR

OSTERLUND, B. R., HAYAKAWA, K., MADSEN, N. B. and JAMES, M. N. G., Crystallization of Glycogen Debranching Enzyme . 557

NUMBER 4, 25 APRIL 1984

KOYODA, H., KOHARA, M., KATAOKA, Y., SUGANUMA, T., OMATA, T., IMURA, N. and NOMOTO, A., Complete Nucleotide Sequences of All Three Poliovirus Serotype Genomes. Implication for Genetic Relationship, Gene Function and Antigenic Determinants 561

LABUDA, D., STRIKER, G. and PORSCHKE, D., Mechanism of Codon Recognition by Transfer RNA and Codon-induced tRNA Association . 587

Chang, Z.-T. (see also Miki, T.), 627
Childs, G. (see also Roberts, S. B.), 647
Chothia, C. (see also Lesk, A. M.), 175
Christen, P. (see also Kirsch, J. F.), 497
Chromosomal excision and integration, SV40, in rat cells, and DNA sequence studies, 55
Circular DNAs, extrachromosomal, containing the *Alu* family of dispersed repetitive sequences and also other regions of chromosomal DNA; a study of structure, 41
— —, extrachromosomal, containing the *Alu* family of dispersed repetitive sequences may be reverse transcripts, 31
Citrate synthase complex with oxaloacetate and *S*-acetonyl-coenzyme A, crystal structure analysis and molecular model, 205
Cleavage of the two yolk proteins from a precursor in *Caenorhabditis elegans*, 419
Cloning of a yolk protein gene family from *Caenorhabditis elegans*, 1
Clore, G. M., Gronenborn, A. M. & McLaughlin, L. W., Structure of the ribonucleoside diphosphate codon UpUpC bound to $tRNA^{Phe}$ from yeast. A time-dependent transferred nuclear Overhauser enhancement study, 163
Codon recognition by tRNA and codon-induced tRNA association, determination of mechanism, 587
— UpUpC bound to yeast $tRNA^{Phe}$, a time-dependent transferred nuclear Overhauser enhancement study of structure, 163
Complex of citrate synthase with oxaloacetate and *S*-acetonyl-coenzyme A, crystal structure analysis and molecular model, 205
Conformations, multiple, coexist and interchange in natural *B* DNA fibers, 221
Conner, B. N., Yoon, C., Dickerson, J. L. & Dickerson, R. E., Helix geometry and hydration in an *A*-DNA tetramer: ^{I}C-C-G-G, 663
Co-operativity, apparent, for highly concentrated Michaelian and allosteric enzymes, 543
Creighton, T. E. (see also States, D. J.), 411
Crosslinking, chemical, of Rous sarcoma virus p19 and gp35 to high molecular weight complexes. An insight into virus assembly, 297
Crystal packing and stoichiometry of the fibre protein of adenovirus type 2, 729
— structure analysis and molecular model of a complex of citrate synthase with oxaloacetate and *S*-acetonyl-coenzyme A, 205
Crystalline sheets of tropomyosin, 231
Crystallization and preliminary X-ray diffraction studies of soybean agglutinin, 723
— of glycogen debranching enzyme, 557
Cytoplasmic mRNA prevalence regulation in sea urchin embryos; rates of appearance and turnover for specific sequences, 85
— space in central nervous system myelin, a model; lipid/myelin basic protein multilayers, 385

Davidson, E. H. (see also Cabrera, C. V.), 85
Debranching enzyme, glycogen; crystallization, 557
Dehydrogenase, NAD(P)H, unspecific, from human erythrocytes, preliminary X-ray studies, 727
Deisenhofer, J. (see also Wiegand, G.), 205
DNA fibers, *B*, natural, have multiple conformations that coexist and interchange, 221
—, ribosomal, rat, characterization; the highly repetitive sequences that flank the rRNA transcription unit are homologous and contain RNA polymerase III transcription initiation sites, 141
—, —, transcription in *Xenopus* oocytes, effect of topological constraint; comparison of plasmid and endogenous genes, 121
— sequence studies of SV40 chromosomal excision and integration in rat cells, 55
DNAs, circular, extrachromosomal, containing the *Alu* family of dispersed repetitive sequences and also other regions of chromosomal DNA; a study of structure, 41
—, —, —, — — — — — — — — — — may be reverse transcripts, 31
A-DNA tetramer, ^{I}C-C-G-G, helix geometry and hydration, 663
B DNA fibers, natural, have multiple conformations that coexist and interchange, 221
Devaux, C., Berthet-Colominas, C., Timmins, P. A., Boulanger, P. & Jacrot, B., Crystal packing and stoichiometry of the fibre protein of adenovirus type 2, 729
Development-specific promoter of *Myxococcus xanthus*, identification, 113
Dickerson, J. L. (see also Conner, B. N.), 663
Dickerson, R. E. (see also Conner, B. N.), 663
Dielectric models applied to the packing of α-helices in globular proteins, 527
Dispersed repetitive sequences, *Alu* family, and the possibility of extrachromosomal circular DNAs being reverse transcripts, 31

— — —, — —, contained in extrachromosomal circular DNAs together with other regions of chromosomal DNA; a study of structure, 41
Disulphide bonds, and a new two-disulphide intermediate in the refolding of reduced bovine pancreatic trypsin inhibitor, 411
DOBSON, C. M. (see also STATES, D. J.), 411
Domain closure mechanism in proteins, 175
DONEGAN, M. (see also BLUMENTHAL, T.), 1
DUX, L. (see also TAYLOR, K.), 193

EICHELE, G. (see also KIRSCH, J. F.), 497
Electron microscopic determination of structure and assembly of haptoglobin polymers, 343
— — — — — — of haptoglobin and the haptoglobin–hemoglobin complex, 319
— microscopy of fine fibrin clots and fine and coarse fibrin films. Observations of fibers in cross-section and in deformed states, 369
Electrostatic interactions in globular proteins. Different dielectric models applied to the packing of α-helices, 527
ELLISON, J. W. (see also CABRERA, C. W.), 85
ENGELMAN, D. M. (see also RAMAKRISHNAN, V.), 265
Enzymes, Michaelian and allosteric, highly concentrated, and apparent co-operativity, 543
Erythrocytes, human, biochemical and ultrastructural characterization of a high molecular weight soluble Mg^{2+}-ATPase, 705
—, —, preliminary X-ray studies on an unspecific NAD(P)H dehydrogenase, 727
Escherichia coli, control of cell division by sex factor F; identification of genes for inhibitor protein and trigger protein on the 42·84–43·6 F segment, 627
— —, — — — — — — — — —; the 42·84–43·6 F segment couples cell division of the host bacteria with replication of plasmid DNA, 605
— —, positions of proteins S14, S18 and S20 in the 30 S ribosomal subunit, 265
— —, transcriptional control of the IS*1* transposition, 251
Eukaryotic RNA, ribonucleoprotein organization; evidence that U1 small nuclear RNA is a ribonucleoprotein when base-paired with pre-messenger RNA *in vivo*, 285
Excision, chromosomal, SV40, and integration in rat cells; DNA sequence studies, 55

FERRY, J. D. (see also MÜLLER, M. F.), 369
Fibre protein of adenovirus type 2, crystal packing and stoichiometry, 729
Fibrin clots, fine, and fine and coarse fibrin films, an electron microscopy study; observations of fibers in cross-section and in deformed states, 369
FORD, G. C. (see also KIRSCH, J. F.), 497
FORRESTER, W. (see also BULLOCK, P.), 55
FRIIS, R. R. (see also GEBHARDT, A.), 297
FUJIWARA, T. (see also SHINDO, H.), 221

Gap junction structures. Structural chemistry inferred from X-ray diffraction measurements on sucrose accessibility and trypsin susceptibility, 449
GEBHARDT, A., BOSCH, J. V., ZIEMIECKI, A. & FRIIS, R. R., Rous sarcoma virus p19 and gp35 can be chemically crosslinked to high molecular weight complexes. An insight into virus assembly, 297
GEHRING, H. (see also KIRSCH, J. F.), 497
Gene identification for inhibitor protein and trigger protein on the 42·84–43·6 F segment; control of cell division by sex factor F in *Escherichia coli*, 627
Genes, cloning of a family encoding the yolk proteins from *Caenorhabditis elegans*, 1
—, histone, late, non-allelic, sequence comparisons with their early stage counterparts; evidence for gene conversion within the sea urchin late stage gene family, 647
—, plasmid and endogenous, a comparison; the effect of topological constraint on transcription of ribosomal DNA in *Xenopus* oocytes, 121
—, storage protein, of *Sarcophaga peregrina*, multi-gene structure, 19
Genomes of all three poliovirus serotypes, complete nucleotide sequences; implication for genetic relationship, gene function and antigenic determinants, 561
Globular proteins and electrostatic interactions; different dielectric models applied to the packing of α-helices, 527
Glutathione reductase, structural relationship to lipoamide dehydrogenase, 483
Glycogen debranching enzyme, crystallization, 557
GOODENOUGH, D. A. (see also MAKOWSKI, L.), 449

Greer, J. (see also Wejman, J. C.), 319, 343
Gronenborn, A. M. (see also Clore, G. M.), 163
Guest, J. R. (see also Rice, D. W.), 483

Hainfeld, J. (see also Wejman, J. C.), 319, 343
Haptoglobin and the haptoglobin–hemoglobin complex, structure determination by electron microscopy, 319
— polymers, structure and assembly by electron microscopy, 343
Harris, J. R., Biochemical and ultrastructural characterization of a high molecular weight soluble Mg^{2+}-ATPase from human erythrocytes, 705
Hayakawa, K. (see also Osterlund, B. R.), 557
Helices, *A* and *B*, torsion angle correlation analysis, 688
Helix geometry and hydration in an *A*-DNA tetramer: ^{1}C-C-G-G, 663
α-Helix packing in globular proteins, and the application of different dielectric models, 527
Hemoglobin–haptoglobin complex, structure by electron microscopy, 319
High molecular weight complexes and the chemical crosslinking of Rous sarcoma virus p19 and gp35; an insight into virus assembly, 297
Histone genes, late, non-allelic, sequence comparisons with their early stage counterparts; evidence for gene conversion within the sea urchin late stage gene family, 647
Höchli, M. (see also Sędzik, J.), 385
Horiuchi, T. (see also Miki, T.), 605, 627
Hovsepian, D. (see also Wejman, J. C.), 319, 343
Huber, R. (see also Wiegand, G.), 205
Human erythrocytes, biochemical and ultrastructural characterization of a high molecular weight soluble Mg^{2+}-ATPase, 705
— —, preliminary X-ray studies on an unspecific NAD(P)H dehydrogenase, 727
Hydration and helix geometry in an *A*-DNA tetramer: ^{1}C-C-G-G, 663

Imura, N. (see also Toyoda, H.), 561
Inouye, S., Identification of a development-specific promoter of *Myxococcus xanthus*, 113
IS*1* transposition in *Escherichia coli*, transcriptional control, 251

Jacrot, B. (see also Devaux, C.), 729
James, M. N. G. (see also Osterlund, B. R.), 557
Jansonius, J. N. (see also Kirsch, J. F.), 497

Karplus, M. (see also States, D. J.), 411
Katagiri, T. (see also Shikama, K.), 697
Kataoka, Y. (see also Toyoda, H.), 561
Kellershohn, N. (see also Laurent, M.), 543
Kirsch, J. F., Eichele, G., Ford, G. C., Vincent, M. G., Jansonius, J. N., Gehring, H. & Christen, P., Mechanism of action of aspartate aminotransferase proposed on the basis of its spatial structure, 497
Kirtland, S. (see also Blumenthal, T.), 1
Kjeldgaard, M. (see also Ramakrishnan, V.), 265
Kochan, J., Carrascosa, J. L. & Murialdo, H., Bacteriophage lambda preconnectors. Purification and structure, 433
Kohara, M. (see also Toyoda, H.), 561
Krolewski, J. J. & Rush, M. G., Some extrachromosomal circular DNAs containing the *Alu* family of dispersed repetitive sequences may be reverse transcripts, 31
—, Schindler, C. W. & Rush, M. G., Structure of extrachromosomal circular DNAs containing both the *Alu* family of dispersed repetitive sequences and other regions of chromosomal DNA, 41
Kuroiwa, A. (see also Tahara, T.), 19

Labuda, D., Striker, G. & Porschke, D., Mechanism of codon recognition by transfer RNA and codon-induced tRNA association, 587
λ (see also Bacteriophage), 433
Laurent, M. & Kellershohn, N., Apparent co-operativity for highly concentrated Michaelian and allosteric enzymes, 543
Lee, J. J. (see also Cabrera, C. V.), 85
Lesk, A. M. & Chothia, C., Mechanisms of domain closure in proteins, 175

pid/myelin basic protein multilayers. A model for the cytoplasmic space in central nervous system myelin, 385
oamide dehydrogenase, structural relationship to glutathione reductase, 483
s, H. (see also SHAANAN, B.), 723
WY, J. (see also POULSEN, F. R.), 239

LAUGHLIN, L. W. (see also CLORE, G. M.), 163
cromomycin and auromomycin, a preliminary X-ray diffraction study, 739
ADSEN, N. B. (see also OSTERLUND, B. R.), 557
g^{2+}-ATPase, soluble, high molecular weight, from human erythrocytes; biochemical and ultrastructural characterization, 705
AKOWSKI, L., CASPAR, D. L. D., PHILLIPS, W. C. & GOODENOUGH, D. A., Gap junction structures. V. Structural chemistry inferred from X-ray diffraction measurements on sucrose accessibility and trypsin susceptibility, 449
ARTONOSI, A. (see also TAYLOR, K.), 193
ATSUMOTO, U. (see also SHINDO, H.), 221
ssenger RNA, cytoplasmic, regulation of prevalence in sea urchin embryos; rates of appearance and turnover for specific sequences, 85
chaelian and allosteric enzymes, highly concentrated, and apparent co-operativity, 543
KI, T., CHANG, Z.-T. & HORIUCHI, T., Control of cell division by sex factor F in *Escherichia coli*. II. Identification of genes for inhibitor protein and trigger protein on the 42·84–43·6 F segment, 627
YOSHIOKA, K. & HORIUCHI, T., Control of cell division by sex factor F in *Escherichia coli*. I. The 42·84–43·6 F segment couples cell division of the host bacteria with replication of plasmid DNA, 605
lecular model of a complex of citrate synthase with oxaloacetate and *S*-acetonyl-coenzyme A, 205
ORE, P. B. (see also RAMAKRISHNAN, V.), 265
ROCZKA, D. H., CASSIDY, B., BUSCH, H. & ROTHBLUM, L. I., Characterization of rat ribosomal DNA. The highly repetitive sequences that flank the ribosomal RNA transcription unit are homologous and contain RNA polymerase III transcription initiation sites, 141
ÜLLER, M. F., RIS, H. & FERRY, J. D., Electron microscopy of fine fibrin clots and fine and coarse fibrin films. Observations of fibers in cross-section and in deformed states, 369
ulti-gene structure of the storage protein genes of *Sarcophaga peregrina*, 19
URIALDO, H. (see also KOCHAN, J.), 433
uscle structure determined by the application of potential energy calculations to X-ray data, with special reference to the configuration of myosin heads, 239
yelin basic protein/lipid multilayers. A model for the cytoplasmic space in central nervous system myelin, 385
yosin head configuration determined from X-ray data using potential energy calculations, 239
yxococcus xanthus, identification of a development-specific promoter, 113

(AD(P)H dehydrogenase, unspecific, from human erythrocytes, preliminary X-ray studies, 727
ATORI, S. (see also TAHARA, T.), 19
OMOTO, A. (see also TOYODA, H.), 561
ucleotide sequences, complete, of all three poliovirus serotype genomes. Implication for genetic relationship, gene function and antigenic determinants, 561

SINATA, M. (see also TAHARA, T.), 19
IATA, T. (see also TOYODA, H.), 561
STERLUND, B. R., HAYAKAWA, K., MADSEN, N. B. & JAMES, M. N. G., Crystallization of glycogen debranching enzyme, 557
verhauser effect: a time-dependent transferred nuclear Overhauser enhancement study of the structure of the ribotrinucleoside diphosphate codon UpUpC bound to $tRNA^{Phe}$ from yeast, 163
xaloacetate complex with citrate synthase and *S*-acetonyl-coenzyme A, crystal structure analysis and molecular model, 205
tymyoglobin, *Aplysia*, with an unusual stability property, 697

acking and stoichiometry of fibre protein crystals of adenovirus type 2, 729
of α-helices in globular proteins, and the application of different dielectric models, 527
AI, E. F., Preliminary X-ray studies on an unspecific NAD(P)H dehydrogenase from human erythrocytes, 727

Pederson, T. (see also Setyono, B.), 285
Phillips, W. C. (see also Makowski, L.), 449
Plasmid and endogenous genes, a comparison; the effect of topological constraint on transcription of ribosomal DNA in *Xenopus* oocytes, 121
Poliovirus serotype genomes, complete nucleotide sequences. Implication for genetic relationship, gene function and antigenic determinants, 561
Porschke, D. (see also Labuda, D.), 587
Potential energy calculations, application to the determination of muscle structure from X-ray data with special reference to the configuration of myosin heads, 239
Poulsen, F. R. & Lowy, J., Application of potential energy calculations to the determination of muscle structure from X-ray data with special reference to the configuration of myosin heads, 239
Preconnectors, bacteriophage lambda; purification and structure, 433
Pre-messenger RNA, and evidence that U1 small nuclear RNA is a ribonucleoprotein when there is base-pairing *in vivo*, 285
Promoter, development-specific, of *Myxococcus xanthus*; identification, 113
Protein, fibre, of adenovirus type 2, crystal packing and stoichiometry, 729
—, storage, genes of *Sarcophaga peregrina*, multi-gene structure, 19
—, yolk, cloning of a family of encoding genes from *Caenorhabditis elegans*, 1
Proteins, mechanisms of domain closure, 175
— S14, S18 and S20, positions in the 30 S ribosomal subunit of *Escherichia coli*, 265
—, yolk, two, cleavage from a precursor in *Caenorhabditis elegans*, 419
Pruitt, S. C. & Reeder, R. H., Effect of topological constraint on transcription of ribosomal DNA in *Xenopus* oocytes. Comparison of plasmid and endogenous genes, 121

Ramakrishnan, V., Capel, M., Kjeldgaard, M., Engelman, D. M. & Moore, P. B., Positions of proteins S14, S18 and S20 in the 30 S ribosomal subunit of *Escherichia coli*, 265
Rat cells, DNA sequence studies of SV40 chromosomal excision and integration, 55
— ribosomal DNA, characterization; the highly repetitive sequences that flank the rRNA transcription unit are homologous and contain RNA polymerase III transcription initiation sites, 141
Reeder, R. H. (see also Pruitt, S. C.), 121
Refolding of reduced bovine pancreatic trypsin inhibitor, a new two-disulphide intermediate, 411
Regulation of cytoplasmic mRNA prevalence in sea urchin embryos; rates of appearance and turnover for specific sequences, 85
Remington, S. (see also Wiegand, G.), 205
RNA, eukaryotic, ribonucleoprotein organization; evidence that U1 small nuclear RNA is a ribonucleoprotein when base-paired with pre-messenger RNA *in vivo*, 285
— polymerase III transcription initiation sites are contained in the homologous highly repetitive sequences that flank the rRNA transcription unit; characterization of rat ribosomal DNA, 141
Ribonucleoprotein organization of eukaryotic RNA; evidence that U1 small nuclear RNA is a ribonucleoprotein when base-paired with pre-messenger RNA *in vivo*, 285
Ribosomal DNA, rat, characterization; the highly repetitive sequences that flank the rRNA transcription unit are homologous and contain RNA polymerase III transcription initiation sites, 141
— — transcription in *Xenopus* oocytes, effect of topological constraint, comparison of plasmid and endogenous genes, 121
— 30 S subunit of *Escherichia coli*, positions of proteins S14, S18 and S20, 265
Ribotrinucleoside diphosphate codon UpUpC bound to $tRNA^{Phe}$ from yeast, a time-dependent transferred nuclear Overhauser enhancement study of structure, 163
Rice, D. W., Schulz, G. E. & Guest, J. R., Structural relationship between glutathione reductase and lipoamide dehydrogenase, 483
Ris, H. (see also Müller, M. F.), 369
Roberts, S. B., Weisser, K. E. & Childs, G., Sequence comparisons of non-allelic late histone genes and their early stage counterparts. Evidence for gene conversion within the sea urchin late stage gene family, 647
Rogers, N. K. & Sternberg, M. J. E., Electrostatic interactions in globular proteins. Different dielectric models applied to the packing of α-helices, 527
Rothblum, L. I. (see also Mroczka, D. H.), 141
Rous sarcoma virus p19 and gp35 can be chemically crosslinked to high molecular weight complexes. An insight into virus assembly, 297
Rush, M. G. (see also Krolewski, J. J.), 31, 41

, S18 and S20 protein positions in the 30 S ribosomal subunit of *Escherichia coli*, 265
cetonyl-coenzyme A with complex of citrate synthase and oxaloacetate, crystal structure analysis and molecular model, 205
MY, T. S. A. (see also SIEKER, L. C.), 739
rcophaga peregrina, multi-gene structure of storage protein genes, 19
rcoplasmic reticulum Ca^{2+}-ATPase, structure of vanadate-induced crystals, 193
HINDLER, C. W. (see also KROLEWSKI, J. J.), 41
HULZ, G. E. (see also RICE, D. W.), 483
urchin embryos, regulation of cytoplasmic mRNA prevalence; rates of appearance and turnover for specific sequences, 85
— late stage gene family, and evidence for gene conversion; sequence comparisons of non-allelic late histone genes and their early stage counterparts, 647
DZIK, J., BLAUROCK, A. E. & HÖCHLI, M., Lipid/myelin basic protein multilayers. A model for the cytoplasmic space in central nervous system myelin, 385
uence comparisons of non-allelic late histone genes and their early stage counterparts. Evidence for gene conversion within the sea urchin late stage gene family, 647
DNA, and SV40 chromosomal excision and integration in rat cells, 55
uences, highly repetitive, that flank the rRNA transcription unit are homologous and contain RNA polymerase III transcription initiation sites; characterization of rat rDNA, 141
nucleotide, complete, of all three poliovirus serotype genomes. Implication for genetic relationship, gene function and antigenic determinants, 561
YONO, B. & PEDERSON, T., Ribonucleoprotein organization of eukaryotic RNA. XXX. Evidence that U1 small nuclear RNA is a ribonucleoprotein when base-paired with pre-messenger RNA *in vivo*, 285
factor F and control of cell division in *Escherichia coli*; identification of genes for inhibitor protein and trigger protein on the 42·84–43·6 F segment, 627
— — — — — — — — —; the 42·84–43·6 F segment couples cell division of the host bacteria with replication of plasmid DNA, 605
AANAN, B., SHOHAM, M., YONATH, A., LIS, H. & SHARON, N., Crystallization and preliminary X-ray diffraction studies of soybean agglutinin, 723
ARON, N. (see also SHAANAN, B.), 723
ARROCK, W. J., Cleavage of two yolk proteins from a precursor in *Caenorhabditis elegans*, 419
ARROCK, W. (see also BLUMENTHAL, T.), 1
KAMA, K. & KATAGIRI, T., *Aplysia* oxymyoglobin with an unusual stability property, 697
MIDZU, M. (see also SHINDO, H.), 221
NDO, H., FUJIWARA, T., AKUTSU, H., MATSUMOTO, U. & SHIMIDZU, M., Multiple conformations coexist and interchange in natural *B* DNA fibers, 221
OHAM, M. (see also SHAANAN, B.), 723
KER, L. C. & SAMY, T. S. A., Structural study of crystalline auromomycin. Preliminary X-ray diffraction study of auromomycin and macromomycin, 739
ian virus 40 chromosomal excision and integration in rat cells, and DNA sequence studies, 55
ybean agglutinin, crystallization and preliminary X-ray diffraction studies, 723
ETH, J. (see also BLUMENTHAL, T.), 1
IRE, M. (see also BLUMENTHAL, T.), 1
bility property, unusual, of *Aplysia* oxymyoglobin, 697
ATES, D. J., DOBSON, C. M., KARPLUS, M. & CREIGHTON, T. E., A new two-disulphide intermediate in the refolding of reduced bovine pancreatic trypsin inhibitor, 411
ERNBERG, M. J. E. (see also ROGERS, N. K.), 527
WART, M., Crystalline sheets of tropomyosin, 231
ichiometry and crystal packing of the fibre protein of adenovirus type 2, 729
rage protein genes of *Sarcophaga peregrina*, multi-gene structure, 19
IKER, G. (see also LABUDA, D.), 587
uctural relationship between glutathione reductase and lipoamide dehydrogenase, 483
study of crystalline auromomycin. Preliminary X-ray diffraction study of auromomycin and macromomycin, 739
ucture analysis and molecular model of a complex of citrate synthase with oxaloacetate and *S*-acetonyl-coenzyme A, 205
and assembly of haptoglobin polymers by electron microscopy, 343
— purification of bacteriophage lambda preconnectors, 433
of extrachromosomal circular DNAs containing both the *Alu* family of dispersed repetitive sequences and other regions of chromosomal DNA, 41

— — haptoglobin and the haptoglobin–hemoglobin complex by electron microscopy, 319
— — muscle determined by the application of potential energy calculations to X-ray data, with special reference to the configuration of myosin heads, 239
— — the ribonucleoside diphosphate codon UpUpC bound to $tRNA^{Phe}$ from yeast. A time-dependent transferred nuclear Overhauser enhancement study, 163
— — — vanadate-induced crystals of sarcoplasmic reticulum Ca^{2+}-ATPase, 193
—, multi-gene, of the storage protein genes of *Sarcophaga peregrina*, 19
—, spatial, as the basis for the mechanism of action of aspartate aminotransferase, 497
Structures of gap junctions. Structural chemistry inferred from X-ray diffraction measurements on sucrose accessibility and trypsin susceptibility, 449
Sucrose accessibility and trypsin susceptibility from X-ray diffraction measurements, and the inferred structural chemistry of gap junctions, 449
Suganuma, T. (see also Toyoda, H.), 561

Tahara, T., Kuroiwa, A., Obinata, M. & Natori, S., Multi-gene structure of the storage protein genes of *Sarcophaga peregrina*, 19
Taylor, K., Dux, L. & Martonosi, A., Structure of the vanadate-induced crystals of sarcoplasmic reticulum Ca^{2+}-ATPase, 193
Time-dependent transferred nuclear Overhauser enhancement study of the structure of the ribotrinucleoside diphosphate codon UpUpC bound to yeast $tRNA^{Phe}$, 163
Timmins, P. A. (see also Devaux, C.), 729
Topological constraint, effect on transcription of ribosomal DNA in *Xenopus* oocytes; comparison of plasmid and endogenous genes, 121
Torsion angle correlation analysis for *A* and *B* helices, 688
Toyoda, H., Kohara, M., Kataoka, Y., Suganuma, T., Omata, T., Imura, N. & Nomoto, A., Complete nucleotide sequence of all three poliovirus serotype genomes. Implication for genetic relationship, gene function and antigenic determinants, 561
Transcription of ribosomal DNA in *Xenopus* oocytes, effect of topological constraint; comparison of plasmid and endogenous genes, 121
— unit, rRNA, the highly repetitive flanking sequences are homologous and contain RNA polymerase III transcription initiation sites; characterization of rat ribosomal DNA, 141
Transcriptional control of IS*1* transposition in *Escherichia coli*, 251
Transcripts, reverse, and some extrachromosomal circular DNAs containing the *Alu* family of dispersed repetitive sequences, 31
Transfer RNA recognition of codons, and codon-induced tRNA association; mechanism determination, 587
$tRNA^{Phe}$ from yeast, bound to the ribotrinucleoside diphosphate codon UpUpC; a time-dependent transferred nuclear Overhauser enhancement study of structure, 163
Transposition, IS*1*, transcriptional control in *Escherichia coli*, 251
Tropomyosin crystalline sheets, 231
Trypsin susceptibility and sucrose accessibility from X-ray diffraction measurements, and the inferred structural chemistry of gap junctions, 449

U1 small nuclear RNA, evidence that it is a ribonucleoprotein when base-paired with pre-messenger RNA *in vivo*, 285
UpUpC bound to $tRNA^{Phe}$ from yeast, a time-dependent transferred nuclear Overhauser enhancement study of structure, 163
Ultrastructural and biochemical characterization of a high molecular weight soluble Mg^{2+}-ATPase from human erythrocytes, 705

Vanadate-induced crystals of sarcoplasmic reticulum Ca^{2+}-ATPase; structure determination, 193
Vincent, M. G. (see also Kirsch, J. F.), 497
Virus, Rous sarcoma, p19 and gp35 can be chemically crosslinked to high molecular weight complexes. An insight into virus assembly, 297
—, simian virus 40, chromosomal excision and integration in rat cells, and DNA sequence studies, 55

Wall, J. S. (see also Wejman, J. C.), 319, 343
Weisser, K. E. (see also Roberts, S. B.), 647
Wejman, J. C., Hovsepian, D., Wall, J. S., Hainfeld, J. F. & Greer, J., Structure and assembly of haptoglobin polymers by electron microscopy, 343

—, —, —, — & —, — of haptoglobin and the haptoglobin–hemoglobin complex by electron microscopy, 319
Viegand, G., Remington, S., Deisenhofer, J. & Huber, R., Crystal structure analysis and molecular model of a complex of citrate synthase with oxaloacetate and *S*-acetonyl-coenzyme A, 205

Xenopus oocytes, effect of topological constraint on transcription of ribosomal DNA; comparison of plasmid and endogenous genes, 121
X-ray data used in potential energy calculations to determine muscle structure, with special reference to the configuration of myosin heads, 239
— diffraction measurements on sucrose accessibility and trypsin susceptibility, and the structural chemistry of gap junctions, 449
— — studies, preliminary, and crystallization, of soybean agglutinin, 723
— — study, preliminary, of auromomycin and macromomycin, 739
— studies, preliminary, on an unspecific NAD(P)H dehydrogenase from human erythrocytes, 727

Yeast $tRNA^{Phe}$ bound to ribotrinucleoside diphosphate codon UpUpC; a time-dependent transferred nuclear Overhauser enhancement study of structure, 163
Yolk protein, cloning of a family of encoding genes from *Caenorhabditis elegans*, 1
— proteins, two, cleavage from a precursor in *Caenorhabditis elegans*, 419
Yonath, A. (see also Shaanan, B.), 723
Yoon, C. (see also Conner, B. N.), 663
Yoshioka, K. (see also Miki, T.), 605

Ziemiecki, A. (see also Gebhardt, A.), 297